RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/018,418A_

Source: _1FW/6_

Date Processed by STIC: _11/15/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 11/15/2004
PATENT APPLICATION: US/10/018,418A   TIME: 11:56:52

Input Set : A:\72715Supplemental.txt
Output Set: N:\CRF4\11152004\J018418A.raw

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   3  <110> APPLICANT: Morrell, Matthew
   4        Li, Zhongyi
   5        Rahman, Sadequr
   6        Appels, Rudolph
   8  <120> TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES THEREFOR
  10  <130> FILE REFERENCE: 72715Supplemental
  12  <140> CURRENT APPLICATION NUMBER: 10/018,418A
  13  <141> CURRENT FILING DATE: 2002-05-09
  15  <160> NUMBER OF SEQ ID NOS: 59
  17  <170> SOFTWARE: PatentIn version 3.1
  19  <210> SEQ ID NO: 1
  20  <211> LENGTH: 2939
  21  <212> TYPE: DNA
  22  <213> ORGANISM: Triticum aestivum
  24  <220> FEATURE:
  25  <221> NAME/KEY: CDS
  26  <222> LOCATION: (176)..(2569)
  27  <223> OTHER INFORMATION:
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P.6

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  33  cccactgccg cgctactccc cactcccact gccaccacct ccgcctgcgc cgcgctctgg     120
  35  gcggaccaac ccgcgcatcg tatcacgatc acccacccg atcccggccg ccgcc atg       178
  36                                                                   Met
  37                                                                     1
  39  tcg tcg gcg gtc gcg tcc gcc gcg tcc ttc ctc gcg ctc gcg tcc gcc      226
  40  Ser Ser Ala Val Ala Ser Ala Ala Ser Phe Leu Ala Leu Ala Ser Ala
  41              5                  10                  15
  43  tcc ccc ggg aga tca cgg agg agg acg agg gtg agc gcg tcg cca ccc      274
  44  Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro Pro
  45              20                  25                  30
  47  cac acc ggg gct ggc agg ttg cac tgg ccg ccg tcg ccg ccg cag cgc      322
  48  His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln Arg
  49          35                  40                  45
  51  acg gct cgc gac gga gcg gtg gcc gcg cgc gcc gcc ggg aag aag gac      370
  52  Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys Asp
  53  50                  55                  60                  65
  55  gcg ggg atc gac gac gcc gcg ccc gcg agg cag ccc cgc gca ctc cgc      418
  56  Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu Arg
  57                  70                  75                  80
  59  ggt ggc gcc gcc acc aag gtt gcg gag cgg agg gat ccc gtc aag acg      466
  60  Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys Thr
  61              85                  90                  95
  63  ctc gat cgc gac gcc gcg gaa ggt ggc gcg ccg tcc ccg ccg gca ccg      514
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 64 Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala Pro
 65         100             105             110
 67 agg cag gag gac gcc cgt ctg ccg agc atg aac ggc atg ccg gtg aac      562
 68 Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val Asn
 69         115             120             125
 71 ggt gaa aac aaa tct acc ggc ggc ggc ggc gcg act aaa gac agc ggg      610
 72 Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser Gly
 73 130             135             140                 145
 75 ctg ccc gca ccc gca cgc gcg ccc cag ccg tcg agc cag aac aga gta      658
 76 Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg Val
 77         150             155             160
 79 ccg gtg aat ggt gaa aac aaa gct aac gtc gcc tcg ccg ccg acg agc      706
 80 Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr Ser
 81         165             170             175
 83 ata gcc gag gtc gcg gct ccg gat ccc gca gct acc att tcc atc agt      754
 84 Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile Ser
 85         180             185             190
 87 gac aag gcg cca gag tcc gtt gtc cca gcc gag aag gcg ccg ccg tcg      802
 88 Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro Ser
 89         195             200             205
 91 tcc ggc tca aat ttc gtg ccc tcg gct tct gct ccc ggg tct gac act      850
 92 Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp Thr
 93 210             215             220                 225
 95 gtc agc gac gtg gaa ctt gaa ctg aag aag ggt gcg gtc att gtc aaa      898
 96 Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val Lys
 97         230             235             240
 99 gaa gct cca aac cca aag gct ctt tcg ccg ccc gca gca ccc gct gta      946
100 Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala Val
101         245             250             255
103 caa caa gac ctt tgg gac ttc aag aaa tac att ggt ttc gag gag ccc      994
104 Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu Pro
105         260             265             270
107 gtg gag gcc aag gat gat ggc cgg gct gtt gca gat gat gcg ggc tcc     1042
108 Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly Ser
109         275             280             285
111 ttc gaa cac cac cag aat cac gat tcc ggg cct ttg gca ggg gag aac     1090
112 Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu Asn
113 290             295             300                 305
115 gtc atg aac gtg gtc gtc gtg gct gct gaa tgt tct ccc tgg tgc aaa     1138
116 Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys Lys
117         310             315             320
119 aca ggt ggt ctt gga gat gtt gcc ggt gct ttg ccc aag gct ttg gcg     1186
120 Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu Ala
121         325             330             335
123 aag aga gga cat cgt gtt atg gtt gtg gta cca agg tat ggg gac tat     1234
124 Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp Tyr
125         340             345             350
127 gag gaa gcc tac gat gtc gga gtc cga aaa tac tac aag gct gct gga     1282
128 Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala Gly
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            Input Set : A:\72715Supplemental.txt
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129     355                    360                    365
131 cag gat atg gaa gtg aat tat ttc cat gct tat atc gat gga gtt gat      1330
132 Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly Val Asp
133 370                    375                    380              385
135 ttt gtg ttc att gac gct cct ctc ttc cga cac cgc cag gaa gac att      1378
136 Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu Asp Ile
137                    390                    395              400
139 tat ggg ggc agc aga cag gaa att atg aag cgc atg att ttg ttc tgc      1426
140 Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu Phe Cys
141               405                    410              415
143 aag gcc gct gtc gag gtt cca tgg cac gtt cca tgc ggc ggt gtc cct      1474
144 Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly Val Pro
145          420                    425              430
147 tat ggg gat gga aat ctg gtg ttt att gca aat gat tgg cac acg gca      1522
148 Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala
149          435                    440              445
151 ctc ctg cct gtc tat ctg aaa gca tat tac agg gac cat ggt ttg atg      1570
152 Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly Leu Met
153 450                    455                    460              465
155 cag tac act cgg tcc att atg gtg ata cat aac atc gct cac cag ggc      1618
156 Gln Tyr Thr Arg Ser Ile Met Val Ile His Asn Ile Ala His Gln Gly
157                    470                    475              480
159 cgt ggc cca gta gat gag ttc ccg ttc acc gag ttg cct gag cac tac      1666
160 Arg Gly Pro Val Asp Glu Phe Pro Phe Thr Glu Leu Pro Glu His Tyr
161               485                    490              495
163 ctg gaa cac ttc aga ctg tac gac ccc gtg ggt ggt gaa cac gcc aac      1714
164 Leu Glu His Phe Arg Leu Tyr Asp Pro Val Gly Gly Glu His Ala Asn
165          500                    505              510
167 tac ttc gcc gcc ggc ctg aag atg gcg gac cag gtt gtc gtc gtg agc      1762
168 Tyr Phe Ala Ala Gly Leu Lys Met Ala Asp Gln Val Val Val Val Ser
169 515                    520                    525
171 ccg ggg tac ctg tgg gag ctg aag acg gtg gag ggc ggc tgg ggg ctt      1810
172 Pro Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly Trp Gly Leu
173 530                    535                    540              545
175 cac gac atc ata cgg cag aac gac tgg aag acc cgc ggc atc gtg aac      1858
176 His Asp Ile Ile Arg Gln Asn Asp Trp Lys Thr Arg Gly Ile Val Asn
177               550                    555              560
179 ggc atc gac aac atg gag tgg aac ccc gag gtg gac gtc cac ctc aag      1906
180 Gly Ile Asp Asn Met Glu Trp Asn Pro Glu Val Asp Val His Leu Lys
181               565                    570              575
183 tcg gac ggc tac acc aac ttc tcc ctg ggg acg ctg gac tcc ggc aag      1954
184 Ser Asp Gly Tyr Thr Asn Phe Ser Leu Gly Thr Leu Asp Ser Gly Lys
185          580                    585              590
187 cgg cag tgc aag gag gcc ctg cag cgg gag ctg ggc ctg cag gtc cgc      2002
188 Arg Gln Cys Lys Glu Ala Leu Gln Arg Glu Leu Gly Leu Gln Val Arg
189          595                    600              605
191 ggc gac gtg ccg ctg ctc ggc ttc atc ggg cgc ctg gac ggg cag aag      2050
192 Gly Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp Gly Gln Lys
193 610                    615                    620              625
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195 ggc gtg gag atc atc gcg gac gcg atg ccc tgg atc gtg agc cag gac    2098
196 Gly Val Glu Ile Ile Ala Asp Ala Met Pro Trp Ile Val Ser Gln Asp
197                 630             635                 640
199 gtg cag ctg gtc atg ctg ggc acc ggg cgc cac gac ctg gag ggc atg    2146
200 Val Gln Leu Val Met Leu Gly Thr Gly Arg His Asp Leu Glu Gly Met
201             645             650                 655
203 ctg cgg cac ttc gag cgg gag cac cac gac aag gtg cgc ggg tgg gtg    2194
204 Leu Arg His Phe Glu Arg Glu His His Asp Lys Val Arg Gly Trp Val
205         660             665                 670
207 ggg ttc tcc gtg cgg ctg gcg cac cgg atc acg gcc ggc gcc gac gcg    2242
208 Gly Phe Ser Val Arg Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ala
209     675             680                 685
211 ctc ctc atg ccc tcc cgg ttc gag ccg tgc gga ctg aac cag ctc tac    2290
212 Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr
213 690             695             700                 705
215 gcc atg gcc tac ggc acc gtc ccc gtc gtg cat gcc gtc ggt ggc ctg    2338
216 Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu
217             710             715                 720
219 agg gac acc gtg ccg ccg ttc gac ccc ttc aac cac tcc ggg ctc ggg    2386
220 Arg Asp Thr Val Pro Pro Phe Asp Pro Phe Asn His Ser Gly Leu Gly
221             725             730                 735
223 tgg acg ttc gac cgc gca gag gcg cag aag ctg atc gag gcg ctc ggg    2434
224 Trp Thr Phe Asp Arg Ala Glu Ala Gln Lys Leu Ile Glu Ala Leu Gly
225         740             745                 750
227 cac tgc ctc cgc acc tac cgg gac tac aag gag agc tgg agg ggg ctc    2482
228 His Cys Leu Arg Thr Tyr Arg Asp Tyr Lys Glu Ser Trp Arg Gly Leu
229     755             760                 765
231 cag gag cgc ggc atg tcg cag gac ttc agc tgg gag cat gcc gcc aag    2530
232 Gln Glu Arg Gly Met Ser Gln Asp Phe Ser Trp Glu His Ala Ala Lys
233 770             775                 780                 785
235 ctc tac gag gac gtc ctc gtc aag gcc aag tac cag tgg tgaacgctag    2579
236 Leu Tyr Glu Asp Val Leu Val Lys Ala Lys Tyr Gln Trp
237             790                 795
239 ctgctagccg gtccagcccc gcatgcgtgc atgacaggat ggaattgcgc attgcgcacg    2639
241 caggaaggtg ccatggagcg ccggcatccg cgaagtacag tgacatgagg tgtgtgtggt    2699
243 tgagacgctg attccgatct ggtccgtagc agagtagagc ggaggtaggg aagcgctcct    2759
245 tgttacaggt atatgggaat gttgttaact tggtattgta atttgttatg ttgtgtgcat    2819
247 tattacagag ggcaacgatc tgcgccggcg caccggccca actgttgggc cggtcgcaca    2879
249 gcagccgttg gatccgaccg cctgggccgt tggatcccac cgaaaaaaaa aaaaaaaaaa    2939
252 <210> SEQ ID NO: 2
253 <211> LENGTH: 798
254 <212> TYPE: PRT
255 <213> ORGANISM: Triticum aestivum
257 <400> SEQUENCE: 2
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260 1               5                   10                  15
263 Ala Ser Pro Gly Arg Ser Arg Arg Arg Thr Arg Val Ser Ala Ser Pro
264             20                  25                  30
267 Pro His Thr Gly Ala Gly Arg Leu His Trp Pro Pro Ser Pro Pro Gln
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268          35                    40                   45
271 Arg Thr Ala Arg Asp Gly Ala Val Ala Ala Arg Ala Ala Gly Lys Lys
272      50                    55                   60
275 Asp Ala Gly Ile Asp Asp Ala Ala Pro Ala Arg Gln Pro Arg Ala Leu
276 65                    70                   75                   80
279 Arg Gly Gly Ala Ala Thr Lys Val Ala Glu Arg Arg Asp Pro Val Lys
280                   85                   90                   95
283 Thr Leu Asp Arg Asp Ala Ala Glu Gly Gly Ala Pro Ser Pro Pro Ala
284              100                   105                   110
287 Pro Arg Gln Glu Asp Ala Arg Leu Pro Ser Met Asn Gly Met Pro Val
288         115                   120                   125
291 Asn Gly Glu Asn Lys Ser Thr Gly Gly Gly Gly Ala Thr Lys Asp Ser
292      130                   135                   140
295 Gly Leu Pro Ala Pro Ala Arg Ala Pro Gln Pro Ser Ser Gln Asn Arg
296 145                   150                   155                   160
299 Val Pro Val Asn Gly Glu Asn Lys Ala Asn Val Ala Ser Pro Pro Thr
300              165                   170                   175
303 Ser Ile Ala Glu Val Ala Ala Pro Asp Pro Ala Ala Thr Ile Ser Ile
304              180                   185                   190
307 Ser Asp Lys Ala Pro Glu Ser Val Val Pro Ala Glu Lys Ala Pro Pro
308         195                   200                   205
311 Ser Ser Gly Ser Asn Phe Val Pro Ser Ala Ser Ala Pro Gly Ser Asp
312      210                   215                   220
315 Thr Val Ser Asp Val Glu Leu Glu Leu Lys Lys Gly Ala Val Ile Val
316 225                   230                   235                   240
319 Lys Glu Ala Pro Asn Pro Lys Ala Leu Ser Pro Pro Ala Ala Pro Ala
320              245                   250                   255
323 Val Gln Gln Asp Leu Trp Asp Phe Lys Lys Tyr Ile Gly Phe Glu Glu
324         260                   265                   270
327 Pro Val Glu Ala Lys Asp Asp Gly Arg Ala Val Ala Asp Asp Ala Gly
328         275                   280                   285
331 Ser Phe Glu His His Gln Asn His Asp Ser Gly Pro Leu Ala Gly Glu
332      290                   295                   300
335 Asn Val Met Asn Val Val Val Val Ala Ala Glu Cys Ser Pro Trp Cys
336 305                   310                   315                   320
339 Lys Thr Gly Gly Leu Gly Asp Val Ala Gly Ala Leu Pro Lys Ala Leu
340              325                   330                   335
343 Ala Lys Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr Gly Asp
344         340                   345                   350
347 Tyr Glu Glu Ala Tyr Asp Val Gly Val Arg Lys Tyr Tyr Lys Ala Ala
348         355                   360                   365
351 Gly Gln Asp Met Glu Val Asn Tyr Phe His Ala Tyr Ile Asp Gly Val
352      370                   375                   380
355 Asp Phe Val Phe Ile Asp Ala Pro Leu Phe Arg His Arg Gln Glu Asp
356 385                   390                   395                   400
359 Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu Phe
360              405                   410                   415
363 Cys Lys Ala Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly Val
364         420                   425                   430
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 1520
Seq#:9; Xaa Pos. 507
Seq#:10; Xaa Pos. 507
Seq#:53; Xaa Pos. 13
Seq#:54; Xaa Pos. 4

VERIFICATION SUMMARY   DATE: 11/15/2004
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L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:470 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:467
L:908 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:905
L:1242 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1239
L:2125 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:2115
L:2250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1488
M:341 Repeated in SeqNo=9
L:2551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:496
L:4183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:4207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
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